

In the specification

1. Please Amend Table 2B on page 28 as follows:

Table 2B Polymerase Domain Mutations in Various DNA Polymerases

Enzyme	Domain (bp)	Domain sequence	Predicted Mutations for Reducing DNA Polymerase Activity#
	DXXSLYP		
Pfu	405-411	DFRALYP	D405 (D405E)
Tgo	404-410	DFRSLYP	D404 (D404E)
KOD	404-410	DFRSLYP	D404 (D404E)
Vent	407-413	DFRSLYP	D407 [(D404E)] <u>D407E</u>
Deep Vent	405-411	DFRSLYP	D405 [(D404E)] <u>D405E</u>
	YXDTDS		
Pfu	539-544	YIDTDG	T542, D543 (T542P; D543G)
Tgo	538-543	YADTDG	T541, D542 (T541P; D542G)
KOD	538-543	YSDDTG	T541, D542 (T541P; D542G)
Vent	541-546	YADTDG	T544, D545 (T544P; D545G)
Deep Vent	539-544	YIDTDG	T542, D543 (T542P; D543G)
	KXY		
Pfu	593-595	KRY	K593 (K593T)
Tgo	592-594	KKY	K592 (K592T)
KOD	592-594	KKY	K592 (K592T)
Vent	595-597	KRY	K595 (K595T)
Deep			

Vent	593-595	KKY	K593 (K593T)
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2. On page 19, before the full paragraph starting with “Enzymes possessing 3’-5’ exonuclease activity” and ends with “Preferably, the enzyme comprising 3’-5’ exonuclease activity is a DNA polymerase,” please add the following text:

--Amino acid sequence of JDF-3 DNA polymerase (Sequence 2 of WO 01/32887):

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Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Asn Gly Lys Pro Val Ile
1           5           10           15
Arg Val Phe Lys Lys Glu Asn Gly Glu Phe Arg Ile Glu Tyr Asp Arg
           20           25           30
Glu Phe Glu Pro Tyr Phe Tyr Ala Leu Leu Arg Asp Asp Ser Ala Ile
           35           40           45
Glu Glu Ile Lys Lys Ile Thr Ala Glu Arg His Gly Arg Val Val Lys
           50           55           60
Val Lys Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Ser Val
65           70           75           80
Glu Val Trp Val Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile
           85           90           95
Arg Asp Lys Ile Arg Lys His Pro Ala Val Ile Asp Ile Tyr Glu Tyr
           100          105          110
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
           115          120          125
Met Glu Gly Glu Glu Glu Leu Lys Leu Met Ser Phe Asp Ile Glu Thr
           130          135          140
Leu Tyr His Glu Gly Glu Glu Phe Gly Thr Gly Pro Ile Leu Met Ile
145          150          155          160

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Ser Tyr Ala Asp Glu Ser Glu Ala Arg Val Ile Thr Trp Lys Lys Ile			
165	170	175	
Asp Leu Pro Tyr Val Glu Val Val Ser Thr Glu Lys Glu Met Ile Lys			
180	185	190	
Arg Phe Leu Arg Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr			
195	200	205	
Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu			
210	215	220	
Lys Leu Gly Val Ser Phe Thr Leu Gly Arg Asp Gly Ser Glu Pro Lys			
225	230	235	240
Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Val			
245	250	255	
His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr			
260	265	270	
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Val Phe Gly Lys Pro Lys Glu			
275	280	285	
Lys Val Tyr Ala Glu Glu Ile Ala Thr Ala Trp Glu Thr Gly Glu Gly			
290	295	300	
Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Arg Val Thr Tyr			
305	310	315	320
Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu			
325	330	335	
Ile Gly Gln Gly Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu			
340	345	350	
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala			
355	360	365	

Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Gly Gly Tyr
370 375 380
Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Asp Asn Ile
385 390 395 400
Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His
405 410 415
Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Ser Tyr Asp
420 425 430
Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe
435 440 445
Ile Pro Ser Leu Leu Gly Asn Leu Leu Glu Glu Arg Gln Lys Ile Lys
450 455 460
Arg Lys Met Lys Ala Thr Leu Asp Pro Leu Glu Lys Asn Leu Leu Asp
465 470 475 480
Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly Tyr
485 490 495
Tyr Gly Tyr Ala Arg Ala Arg Trp Tyr Cys Arg Glu Cys Ala Glu Ser
500 505 510
Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Met Val Ile Arg Glu Leu
515 520 525
Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ala Asp Thr Asp Gly Leu
530 535 540
His Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala
545 550 555 560
Met Glu Phe Leu Asn Tyr Ile Asn Pro Lys Leu Pro Gly Leu Leu Glu
565 570 575
Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys Lys

580	585	590	
Lys Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Thr Thr Arg Gly Leu			
595	600	605	
Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala			
610	615	620	
Arg Val Leu Glu Ala Ile Leu Arg His Gly Asp Val Glu Glu Ala Val			
625	630	635	640
Arg Ile Val Arg Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro			
645	650	655	
Pro Glu Lys Leu Val Ile His Glu Gln Ile Thr Arg Glu Leu Lys Asp			
660	665	670	
Tyr Lys Ala Thr Gly Pro His Val Ala Ile Ala Lys Arg Leu Ala Ala			
675	680	685	
Arg Gly Val Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu			
690	695	700	
Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe			
705	710	715	720
Asp Pro Thr Lys His Lys Tyr Asp Ala Asp Tyr Tyr Ile Glu Asn Gln			
725	730	735	
Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys			
740	745	750	
Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp			
755	760	765	
Leu Lys Pro Lys Gly Lys Lys Lys (SEQ ID NO: 10)			
770	775		

--Nucleotide sequence of JDF-3 DNA polymerase (Sequence 1 of WO 01/32887)

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atgatccttg acgttgatta catcaccgag aatggaaaagc ccgtcatcag ggtcttcaag      60
aaggagaacg gcgagttcag gattgaatac gaccgcgagt tcgagcccta cttctacgcg      120
ctcctcaggg acgactctgc catcgaagaa atcaaaaaga taaccgcgga gaggcacggc      180
agggtcgtta aggttaagcg cgcggagaag gtgaagaaaa agttcctcgg caggtctgtg      240
gaggtctggg tcctctactt cacgcacccg caggacgttc cggcaatccg cgacaaaata      300
aggaagcacc ccgcggtcac cgacatctac gagtacgaca tacccttcgc caagcgctac      360
ctcatagaca agggcctaata cccgatggaa ggtgaggaag agcttaaact catgtccttc      420
gacatcgaga cgctctacca cgagggagaa gagtttgaa ccgggccgat tctgatgata      480
agctacgccg atgaaagcga ggcgcgcgtg ataacctgga agaagatcga ccttccttac      540
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tatccagtca taaggcgcac cataaacctc ccgacctaca cccttgaggc tgtatacgag      840
gcgggttttcg gcaagcccaa ggagaagggtc tacgccgagg agatagccac cgcctgggag      900
accggcgagg ggcttgagag ggtcgcgcgc tactcgatgg aggacgcgag ggttacctac      960
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atcgaaatgg tcatcagaga gcttgaggaa aagttcggtt ttaaagtcct ctatgcagac	1620
acagacggtc tccatgccac cattcctgga gcggacgctg aaacagtcaa gaaaaaggca	1680
atggagttct taaactatat caatcccaaa ctgcccggcc ttctcgaact cgaatacgag	1740
ggcttctacg tcaggggctt cttcgtcacg aagaaaaagt acgcggtcat cgacgaggag	1800
ggcaagataa ccacgcgcgg gcttgagata gtcaggcgcg actggagcga gatagcgaag	1860
gagacgcagg cgaggggttt ggaggcgata ctcaggcacg gtgacgttga agaggccgtc	1920
agaattgtca gggaagtcac cgaaaagctg agcaagtacg aggttccgcc ggagaagctg	1980
gttatccacg agcagataac gcgcgagctc aaggactaca aggccaccgg cccgcacgta	2040
gccatagcga agcgtttggc cgccagaggt gttaaaatcc ggcccggaac tgtgataagc	2100
tacatcgttc tgaagggtc cggaaggata ggcgacaggc cgattccctt cgacgagttc	2160
gacccgacga agcacaagta cgatgcggac tactacatcg agaaccaggt tctgccggca	2220
gttgagagaa tcctcagggc cttcggtac cgcaagggaag acctgcgcta ccagaagacg	2280
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